Please enter the following amendments and remarks.

Listing of the claims:

What is claimed is:

1. - 48. (Canceled)

49. (Currently amended) A method for detecting Chagas disease in a human test subject, <u>said method</u> comprising:

   a) ~~Q~~quantifying ~~in RNA of a blood sample from said test subject,~~ a level of RNA encoded by ~~the gene~~ <u>an</u> CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A) <u>gene</u> in ~~said~~ <u>a blood</u> sample <u>of said test subject</u>; ~~and~~

   b) ~~C~~comparing said ~~quantified~~ level <u>of RNA in said sample of said test subject</u> with a quantified level of control RNA encoded by said gene ~~and detected~~ in ~~RNA of~~ blood samples ~~from~~<u>of</u> control subjects <u>which are classified as healthy control subjects; and</u>

   <u>c) comparing said level of RNA in said sample of said test subject with a quantified level of control RNA encoded by said gene in blood samples of control subjects which are classified as having Chagas disease;</u>

   wherein ~~said comparison of~~ <u>a statistically significant determination with a p value less than 0.05 resulting from steps (b) and (c) that expression of</u> said ~~quantified level of step (a) with~~ <u>gene in said sample of said test subject is higher with a fold-change of at least 1.5 relative to</u> ~~said quantified level of~~ <u>said samples of</u> said control ~~RNA~~<u>subjects classified as healthy control subjects, and is similar relative to said samples of said control subjects classified as having Chagas disease</u> is indicative of chagas disease in said human test subject.

50. (Currently amended) The method of claim 49, wherein said blood sample of ~~step (a)~~<u>said test subject</u> and said blood samples ~~from~~<u>of</u> said control subjects ~~in step (b)~~ <u>are selected from the group consisting of whole blood samples, blood samples which</u> have not been fractionated

into cell types~~ and blood samples which comprise leukocytes which have not been fractionated into cell types~~.

51. (Cancelled)

52. (Currently amended) The method of ~~any of~~ claims 49~~, 50 or 51~~, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene in ~~step (a)~~ said sample of said test subject is effected ~~by quantifying said RNA~~ relative to a housekeeping gene.

53. (Currently amended) The method of ~~any of~~ claims 49~~, 50 or 51~~, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene in said sample of said test subject ~~in step (a)~~ is effected by quantification of cDNA ~~corresponding~~ complementary to ~~said~~ RNA encoded by said gene.

54. (Cancelled)

55. (Canceled)

56. (Currently Amended) The method of ~~any of~~ claims 49~~, 50 or 51~~, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene ~~in step (a)~~ is ~~determined~~ effected using quantitative ~~real-time RT-~~ PCR.

57. (Currently amended) The method of ~~any of~~ claims 49~~, 50 or 51~~, wherein said quantifying of said level of ~~said~~ RNA encoded by said gene ~~in step (a)~~ is ~~determined~~ effected using an array.

58. (New) A method for detecting expression of an CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A) gene in a human test subject, said method comprising detecting RNA encoded by said gene in a blood sample of said test subject, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene in said sample, and/or for cDNA complementary to RNA encoded by said gene in said sample.

59. (New) The method of claim 58, wherein said detecting of RNA comprises producing an amplification product from RNA encoded by said gene in said blood sample of said test subject, using primers specific only for RNA encoded by said gene and/or for cDNA complementary to RNA encoded by said gene.

60. (New) The method of claim 58 or claim 59, further comprising quantifying a level of RNA encoded by said gene in said sample.

61. (New) The method of claim 60, further comprising comparing said level of RNA to a quantified level of control RNA encoded by said gene in blood samples of control subjects.

62. (New) The method of claim 61, wherein said control subjects are selected from the group consisting of: subjects classified as healthy subjects and subjects classified as having Chagas disease.

63. (New) The method of claim 62, wherein said control subjects are classified as healthy subjects.

64. (New) The method of claim 63, further comprising classifying said test subject as being a candidate for having Chagas disease if said level of RNA encoded by said gene in said blood sample of said human test subject is statistically higher with a fold-change of at least 1.5 and with a p value less than 0.05 relative to that of said control subjects classified as healthy subjects.

65. (New) The method of claim 63, wherein said gene is statistically more highly expressed with a fold-change of at least 1.5 and with a p value less than 0.05 in said blood sample of said human test subject relative to said samples of said control subjects classified as healthy subjects.

66. (New) A method of screening a human test subject for being a candidate for having Chagas disease, said method comprising:

(a) detecting RNA encoded by an CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A) gene in a blood sample of said test subject, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene in said sample, and/or for cDNA complementary to RNA encoded by said gene in said sample; and

(b) quantifying a level of RNA encoded by said gene in said sample of said test subject; and

(c) comparing said level of RNA in said sample of said test subject to a quantified level of control RNA encoded by said gene in blood samples of control subjects classified as healthy subjects;

wherein said test subject is a candidate for having Chagas disease if said level of RNA encoded by said gene in said blood sample of said test subject is statistically higher with a fold change of at least 1.5 and with a p value less than 0.05 relative to said level of RNA encoded by said gene in said samples of said control subjects classified as healthy subjects.

67. (New) The method of claim 58, 59 or 66, wherein said blood sample is selected from the group consisting of: a whole blood sample, a blood sample which has not been fractionated into cell types, and a blood sample which comprises leukocytes which have not been fractionated into cell types.

68. (New) The method of claim 60, wherein said blood sample is selected from the group consisting of: a whole blood sample, a blood sample which has not been fractionated into cell types, and a blood sample which comprises leukocytes which have not been fractionated into cell types.

69. (New) The method of claim 61, wherein:

(i) said blood sample of said test subject and said blood samples of said control subjects are whole blood samples; or

(ii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which have not been fractionated into cell types; or

(iii) said blood sample of said test subject and said blood samples of said control subjects are blood samples which comprise leukocytes which have not been fractionated into cell types.

70. (New) A method of classifying CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A) gene expression in a human test subject, said method comprising:

(a) quantifying a level of RNA encoded by said gene in a blood sample of said test subject;

(b) comparing said level in said sample of said test subject with a quantified level of RNA encoded by said gene in blood samples of control subjects classified as having Chagas disease; and

(c) comparing said level in said sample of said test subject with a quantified level of RNA encoded by said gene in blood samples of control subjects classified as healthy subjects;

wherein a statistically significant determination with a p value less than 0.05 from steps (b) and (c) that said level in said sample of said test subject is similar to said level in said samples of said subjects classified as having Chagas disease and is higher with a fold-change of at least 1.5 relative to said level in said samples of said subjects classified as healthy subjects, results in a classification of CDC14A gene expression in said test subject with that of said subjects classified as having Chagas disease, and

wherein a statistically significant determination with a p value less than 0.05 from steps (b) and (c) that said level in said sample of said test subject is lower with said fold-change relative to said level in said samples of said subjects classified as having Chagas disease and is similar to said level in said samples of said subjects classified as healthy subjects, results in a classification of CDC14A gene expression in said test subject with that of said subjects classified as healthy subjects.

71. (New) The method of claim 60, wherein said quantifying of said level of RNA encoded by said gene is effected by quantifying said level of RNA relative to a housekeeping gene.

72. (New) The method of claim 60, wherein said quantifying of said level of RNA encoded by said gene is effected by quantification of cDNA complementary to RNA encoded by said gene.

73. (New) The method of claim 61, wherein said control subjects do not have Chagas disease.

74. (New) The method of claim 60, wherein said quantifying of said level of RNA encoded by said gene is effected using quantitative PCR.

75. (New) The method of claim 60, wherein said quantifying of said level of RNA encoded by said gene is effected using an array.

76. (New) A method of identifying a CDC14 cell division cycle 14 homolog A (S. cerevisiae) (CDC14A) gene as a candidate biomarker for Chagas disease in a human subject, comprising:

    (a) detecting RNA encoded by said gene in blood samples of human patients diagnosed as having Chagas disease, using an oligonucleotide of predetermined sequence which is specific only for RNA encoded by said gene, and/or for cDNA complementary to RNA encoded by said gene in said samples; and

    (b) quantifying a level of RNA encoded by said gene detected in step (a); and

    (c) comparing said level of RNA quantified in step (b) to a quantified level of control RNA encoded by said gene in blood samples of healthy control subjects;

wherein said gene is a candidate biomarker for Chagas disease in a human subject if said level of RNA encoded by said gene in said blood samples of said human patients diagnosed as having Chagas disease is higher with a fold-change of at least 1.5 relative to said level of RNA in said samples of said healthy control subjects with a p value less than 0.05.

77. (New) The method of claim 76, wherein said blood samples of said human patients diagnosed as having schizophrenia and said blood samples of said healthy control subjects are:

    (i) whole blood samples; or

    (ii) blood samples which have not been fractionated into cell types; or

    (iii) blood samples which comprise leukocytes which have not been fractionated into cell types.

78. (New) The method of claim 76, wherein said quantifying of said level of RNA encoded by said gene is effected by:

    (i) quantifying said level of RNA relative to a housekeeping gene; or

    (ii) quantification of cDNA complementary to RNA encoded by said gene; or

    (iii) using quantitative RT-PCR; or

    (iv) using an array.

79. (New) The method of claim 60, wherein said quantifying of said level of RNA encoded by said gene in said sample of said test subject is effected relative to a housekeeping gene.

80. (New) The method of any of claim 60, wherein said quantifying of said level of RNA encoded by said gene in said sample of said test subject is effected by quantification of cDNA complementary to RNA encoded by said gene.

81. (New) The method of claim 60, wherein said quantifying of said level of RNA encoded by said gene- is effected using quantitative PCR.

82. (New) The method of claim 60, wherein said quantifying of said level of RNA encoded by said gene- is effected using an array.

83. (New) The method of claim 58, 66, 70, 76 or 77, wherein said human test subject is suspected of having Chagas disease.

84. (New) The method of claim 49, 66, 70 or 76, wherein said fold-change is 2 or less.

85. (New) The method of claim 64, wherein said fold-change is 2 or less.

86. (New) The method of claim 65, wherein said fold-change is 2 or less.

87. (New) The method of any one of claims 49, 66, 70 or 76, wherein said fold change is 1.47 or 1.95.